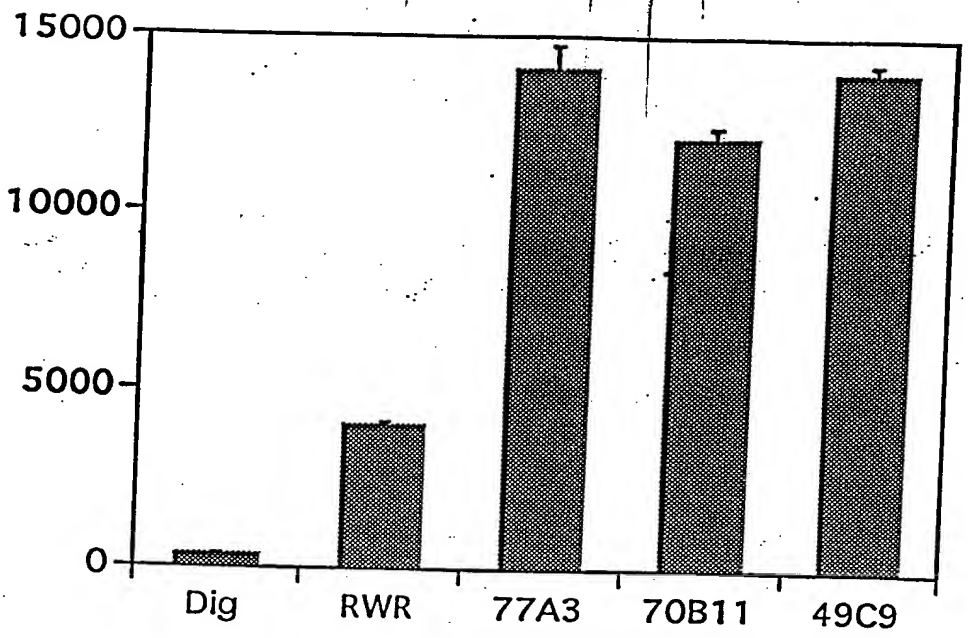
15000
10000
5000
0
Bound a2-Antiplasmin (cpm)
Dig
RWR
77A3
70B11
49C9

FIGURE 1

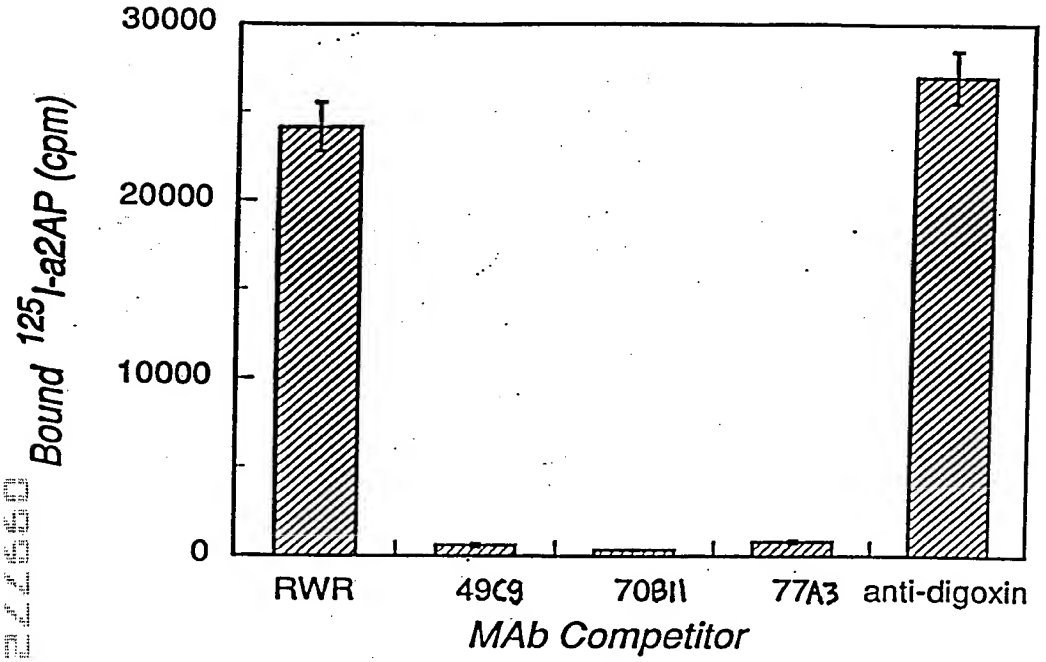
30000
20000
10000
0
Bound ^{125}I-a2AP (cpm)
RWR
49C9
70B11
77A3
anti-digoxin
MAb Competitor

FIGURE 2

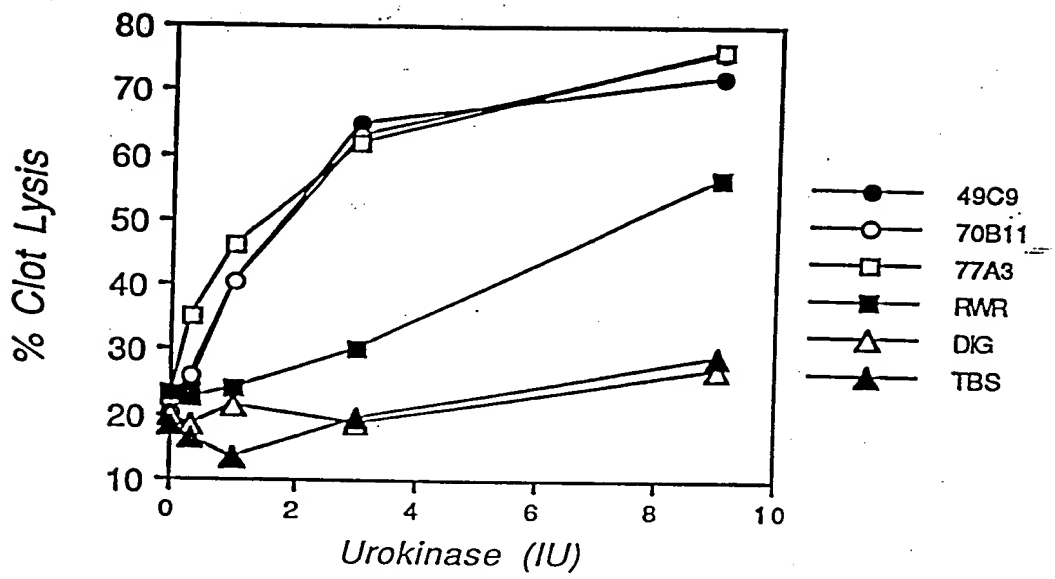
% Clot Lysis
80
70
60
50
40
30
20
10
0
2
4
6
8
10
Urokinase (IU)
49C9
70B11
77A3
RWR
DIG
TBS

FIGURE 3

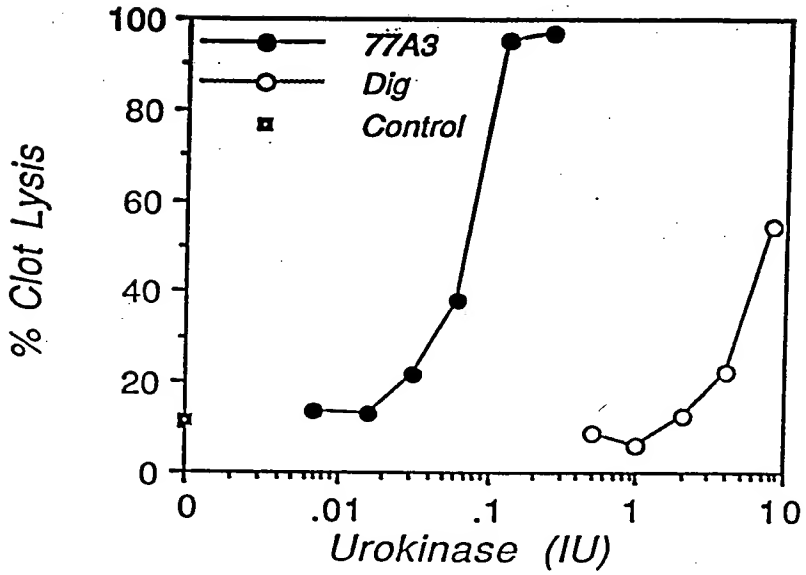
100
80
60
40
20
0
% Clot Lysis
77A3
Dig
Control
0
.01
.1
1
10
Urokinase (IU)

FIGURE 4

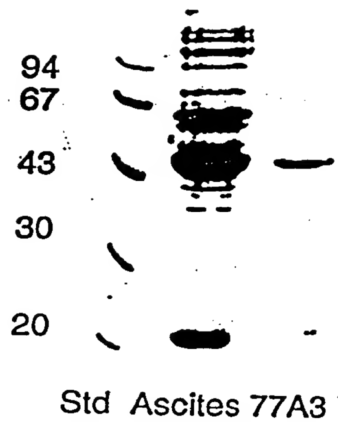

FIGURE 5

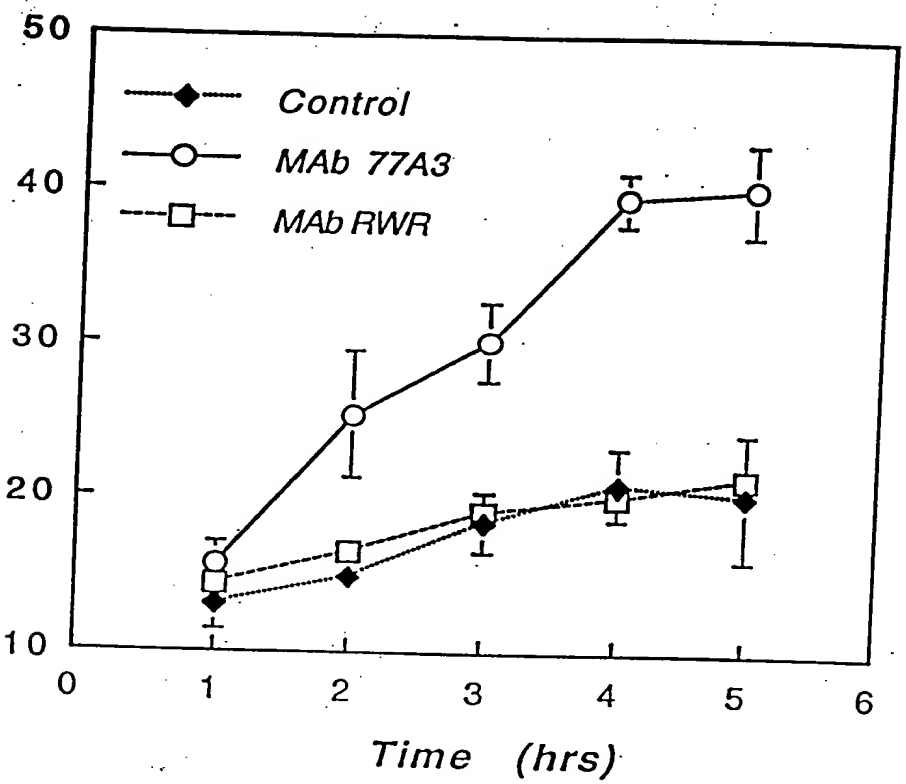
50
40
30
20
10
0
1
2
3
4
5
6
Control
MAb 77A3
MAb RWR
Percent Lysis
Time (hrs)

FIGURE 6

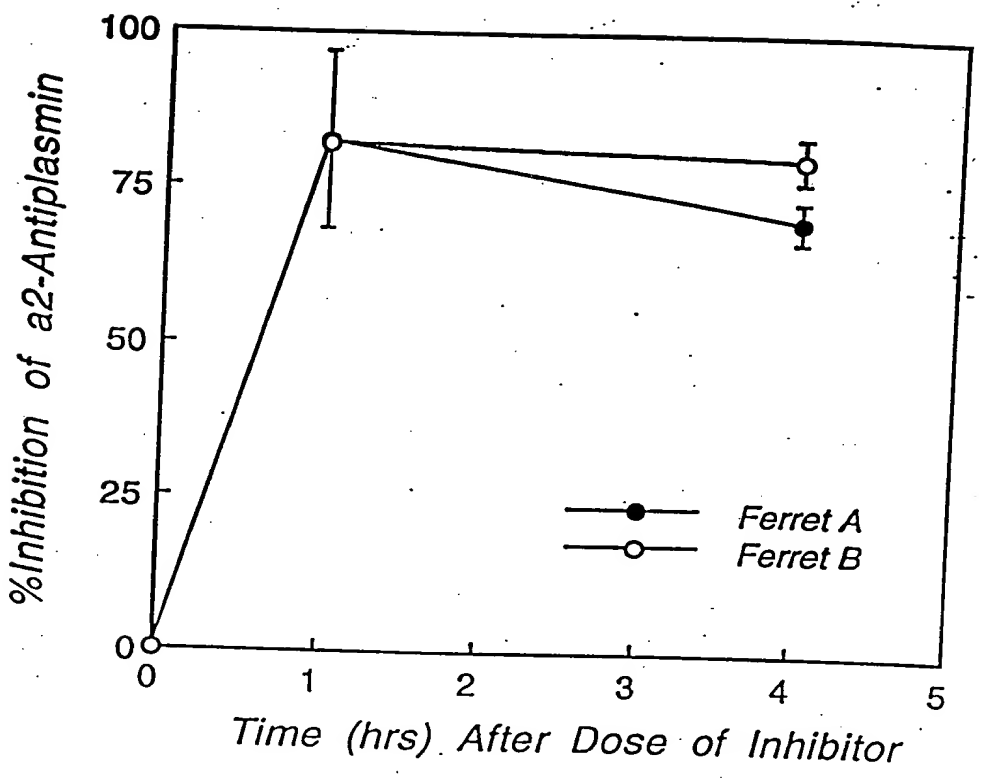

FIGURE 7

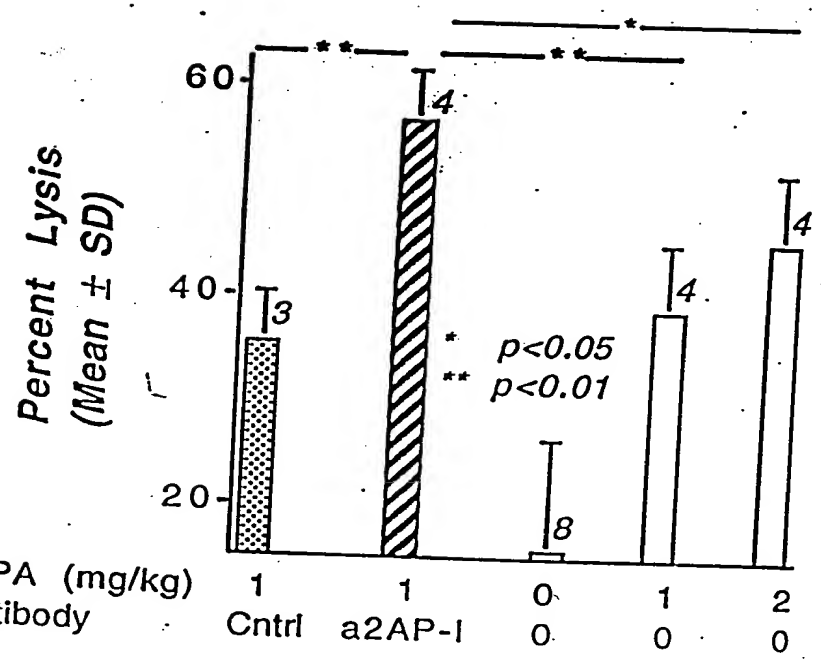
Percent Lysis
(Mean ± SD)
60
40
20
4
3
4
4
8
* p<0.05
** p<0.01
rt-PA (mg/kg)
Antibody
1
Cntrl
1
a2AP-I
0
0
1
0
2
0

FIGURE 8

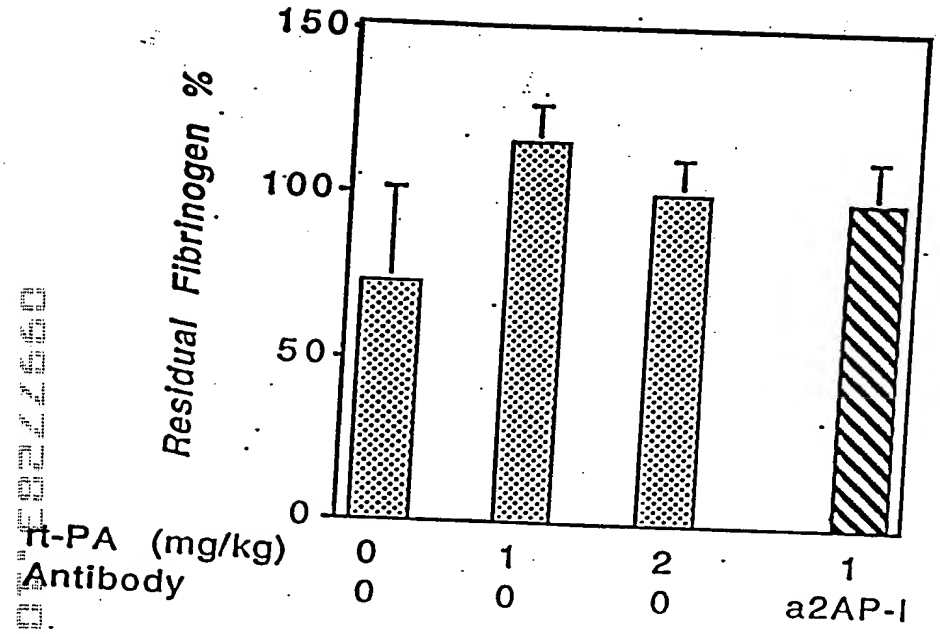
150
100
50
0
Residual Fibrinogen %
rt-PA (mg/kg)
Antibody
0
0
1
0
2
0
1
a2AP-I

FIGURE 9

FIG. 10

MAb Light Chain	Amino Terminal Sequence
49C9	xIQMTQSPASLSASV
70B11	DIQMT
77A3	xIQMTQSPASLSASV

Fig. 11

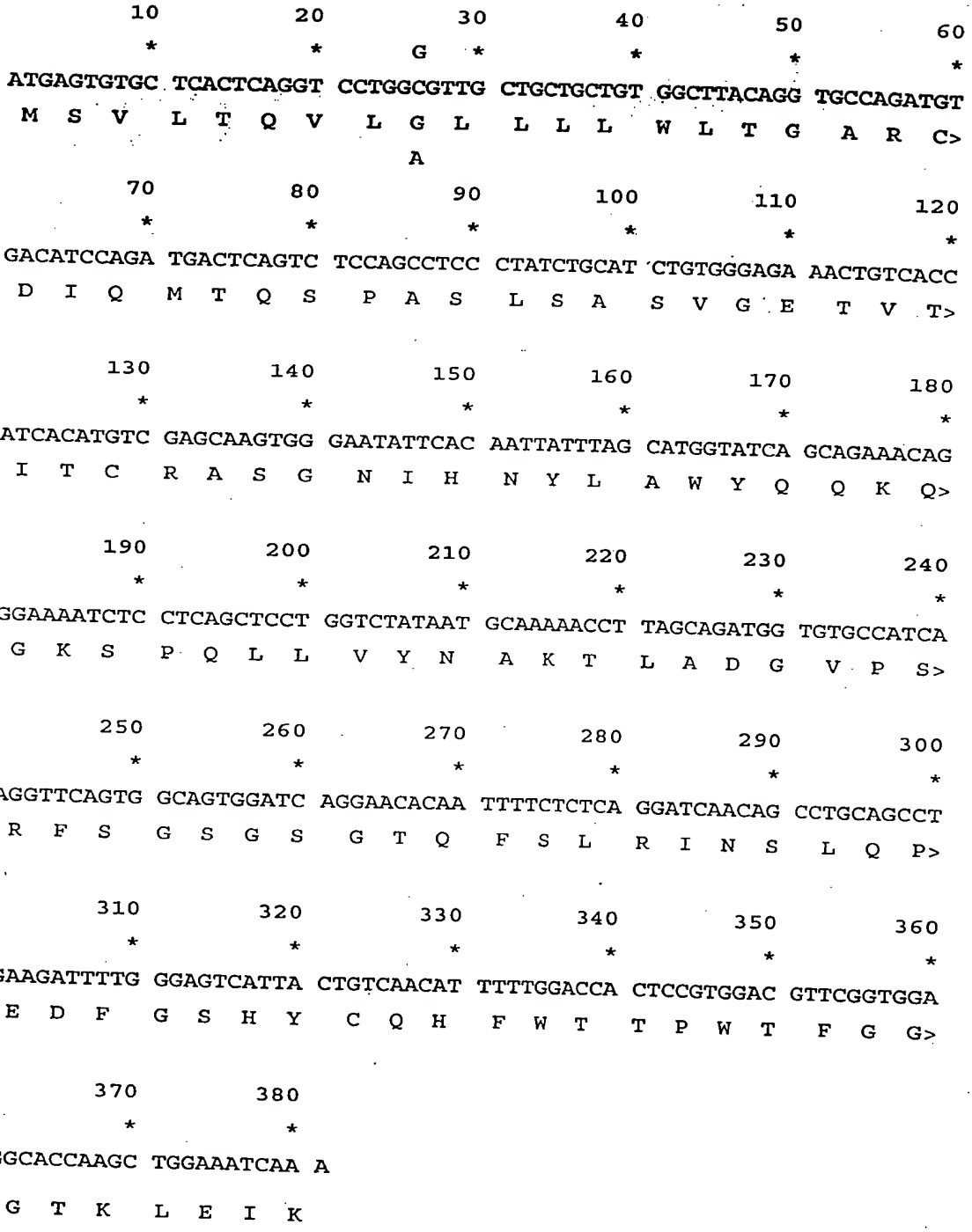

Fig. 12

```
          10         20         30         40         50         60
           *          *          *          *          *          *
ATGAGTGTGC TCACTCAGGT CCTGGGGTTG CTGCTGCTGT GGCTTACAGG TGCCAGATGT
 M  S  V   L  T  Q  V   L  G  L   L  L  L   W  L  T  G   A  R  C>

          70         80         90        100        110        120
           *          *          *          *          *          *
GACATCCAGA TGACTCAGTC TCCAGCCTCC CTATCTGCAT CTGTGGGAGA AACTGTCACC
 D  I  Q   M  T  Q  S   P  A  S   L  S  A   S  V  G  E   T  V  T>

         130        140        150        160        170        180
           *          *          *          *          *          *
GTCACATGTC GAGCAAGTGG GAATATTCAC AATTATTTAG CATGGTATCA GCAGAAACAG
 V  T  C   R  A  S  G   N  I  H   N  Y  L   A  W  Y  Q   Q  K  Q>

         190        200        210        220        230        240
           *          *          *          *          *          *
GGAAAATCTC CTCAGCTCCT GGTCTATAAT GCAAGAACCT TAGCAGATGG TGTGCCATCA
 G  K  S   P  Q  L  L   V  Y  N   A  R  T   L  A  D  G   V  P  S>

         250        260        270        280        290        300
           *          *          *          *          *          *
AGGTTCAGTG GCAGTGGATC AGGAACACAA TATTCTCTCA AGATCAACAG CCTGCAGCCT
 R  F  S   G  S  G  S   G  T  Q   Y  S  L   K  I  N  S   L  Q  P>

         310        320        330        340        350        360
           *          *          *          *          *          *
GAAGATTTTG GGAGTTATTA CTGTCAACAT TTTTGGAGTA ATCCGTGGAC GTTCGGTGGA
 E  D  F   G  S  Y  Y   C  Q  H   F  W  S   N  P  W  T   F  G  G>

         370        380
           *          *
GGCACCAAGC TGGAAATCAA
 G  T  K   L  E  I  K
```

FIG. 13

```
          10          20          30          40          50          60
           *           *           *           *           *           *
ATGAGTGTGC TCACTCAGGT CCTGGCGTTG CTGCTGCTGT GGCTTACAGG TGCCAGATGT
 M  S  V   L  T  Q  V   L  A  L   L  L  L   W  L  T  G   A  R  C>

          70          80          90         100         110         120
           *           *           *           *           *           *
GACATCCAGA TGACTCAGTC TCCAGCCTCC CTATCTGCAT CTGTGGGAGA AACTGTCACC
 D  I  Q   M  T  Q  S   P  A  S   L  S  A   S  V  G  E   T  V  T>

         130         140         150         160         170         180
           *           *           *           *           *           *
ATCACATGTC GAGCAAGTGG GAATATTCAC AATTATTTAG CATGGTATCA GCAGAAACAG
 I  T  C   R  A  S  G   N  I  H   N  Y  L   A  W  Y  Q   Q  K  Q>

         190         200         210         220         230         240
           *           *           *           *           *           *
GGAAAATCTC CTCAACTCCT GGTCTATAAT GCAAAAACCT TAGCAGATGG TGTGCCATCA
 G  K  S   P  Q  L  L   V  Y  N   A  K  T   L  A  D  G   V  P  S>

         250         260         270         280         290         300
           *           *           *           *           *           *
AGGTTCAGTG GCAGTGGATC AGGAACACAA TTTTCTCTCA AGATCAACAG CCTGCAGCCT
 R  F  S   G  S  G  S   G  T  Q   F  S  L   K  I  N  S   L  Q  P>

         310         320         330         340         350         360
           *           *           *           *           *           *
GAAGATTTTG GGAGTCATTA CTGTCAACAT TTTTGGACCA CTCCGTGGAC GTTCGGTGGA
 E  D  F   G  S  H  Y   C  Q  H   F  W  T   T  P  W  T   F  G  G>

         370         380
           *           *
GGCACCAAGC TGGAAATCAA A
 G  T  K   L  E  I  K
```

H2 HC (49c9 heavy chain) Fig. 14

```
          9         19         29         39         49         59
          *          *          *          *          *          *
ATGGMTTGG GTGTGGAMCT TGCTATTCCT GATGGCAGCT GCCCAAAGTC TCCAAGCACA
 M  A  W   V  W  N   L  L  F  L   M  A  A   A  Q  S   L  Q  A  Q>
    D            T
         69         79         89         99        109        119
          *          *          *          *          *          *
GATCCAGTTG GTGCAGTCTG GACCTGAGCT GAAGAAGCCT GGAGAAACAG TCAAGATCTC
  I  Q  L   V  Q  S   G  P  E  L   K  K  P   G  E  T   V  K  I  S>

        129        139        149        159        169        179
          *          *          *          *          *          *
CTGCAAGGCC TCTGGGTATA CCTTCACAAA CTATGGAATG AACTGGGTGA AGCAGGCTCC
  C  K  A   S  G  Y   T  F  T  N   Y  G  M   N  W  V   K  Q  A  P>

        189        199        209        219        229        239
          *          *          *          *          *          *
AGGAAAGGGT TTAAAGTGGA TGGGCTGGAT AAACACCAAG AGTGGAGAGC CAACATATGC
  G  K  G   L  K  W   M  G  W  I   N  T  K   S  G  E   P  T  Y  A>

        249        259        269        279        289        299
          *          *          *          *          *          *
TGAAGAGTTC AAGGGACGGT TTGTCTTCTC TTTGGAAACC TCTGCCAGCA CTGCCCATTT
  E  E  F   K  G  R   F  V  F  S   L  E  T   S  A  S   T  A  H  L>

        309        319        329        339        349        359
          *          *          *          *          *          *
GCAGATCAAG AATTTCAGAA ATGAGGACAC GGCTACATAT TTCTGTGCAA GATGGGTACC
  Q  I  K   N  F  R   N  E  D  T   A  T  Y   F  C  A   R  W  V  P>

        369        379        389        399        409
          *          *          *          *          *
TGGGACCTAT GCTATGGACT ACTGGGGTCA AGGAACCTCA GTCACCGTCT CCTCA
  G  T  Y   A  M  D   Y  W  G  Q   G  T  S   V  T  V   S  S>
```

H3 HC (70B11 heavy chain) Fig. 15

```
         10         20         30         40         50         60
          *          *          *          *          *          *
ATGGMTTGGG TGTGGAMCTT GCTATTCCTG ATGGCAGCTG CCCAAAGTAT CCAAGCACAG
 M  A  W    V  W  N  L   L  F  L   M  A  A   A  Q  S  I   Q  A  Q>
    D             T
         70         80         90        100        110        120
          *          *          *          *          *          *
ATCCAGTTGG TGCAGTCTGG ACCTGAGCTG AAGAAGCCTG GAGAGACAGT CAAGATCTCC
 I  Q  L    V  Q  S  G   P  E  L   K  K  P   G  E  T  V   K  I  S>

        130        140        150        160        170        180
          *          *          *          *          *          *
TGCAAGGCTT CTGGGTATAC CTTCACAAAG TATGGAATGA ACTGGGTGAA GCAGGCTCCA
 C  K  A    S  G  Y  T   F  T  K   Y  G  M   N  W  V  K   Q  A  P>

        190        200        210        220        230        240
          *          *          *          *          *          *
GGAAAGGGTT TAAAGTGGAT GGGCTGGATA AACACCAACA GTGGAGAGCC AACATATGCT
 G  K  G    L  K  W  M   G  W  I   N  T  N   S  G  E  P   T  Y  A>

        250        260        270        280        290        300
          *          *          *          *          *          *
GAAGAGTTCA AGGGACGGTT TGCCTTCTCT TTGGAAACCT CTGCCAGCAC TGCCTATTTG
 E  E  F    K  G  R  F   A  F  S   L  E  T   S  A  S  T   A  Y  L>

        310        320        330        340        350        360
          *          *          *          *          *          *
CAGATCAACA ACCTCAAAAA TGAGGACTCG GCTACATATT TCTGTGCAAG ATGGGTACCT
 Q  I  N    N  L  K  N   E  D  S   A  T  Y   F  C  A  R   W  V  P>

        370        380        390        400        410
          *          *          *          *          *
GGGACCTATG CTATGGACTA CTGGGGTCAA GGAACCTCAG TCACCGTCTC CTCA
 G  T  Y    A  M  D  Y   W  G  Q   G  T  S   V  T  V  S   S>
```

H4 HC (77A3 heavy chain) Fig. 16

```
          10          20          30          40          50          60
           *           *           *           *           *           *
ATGGMTTGGG TGTGGAMCTT GCTATTCCTG ATGGCAGCTG CCCAAAGTAT CCAAGCACAG
 M  A  W   V  W  N  L   L  F  L   M  A  A   A  Q  S  I   Q  A  Q>
    D           T

          70          80          90         100         110         120
           *           *           *           *           *           *
ATCCAGTTGG TGCAGTCTGG ACCTGAGCTG AAGAAGCCTG GAGAAACAGT CAAGATCTCC
 I  Q  L   V  Q  S  G   P  E  L   K  K  P   G  E  T  V   K  I  S>

         130         140         150         160         170         180
           *           *           *           *           *           *
TGCAAGGCTT CTGGGTATAC CTTCACAAAC TATGGAATGA ACTGGGTGAA GCAGGCTCCA
 C  K  A   S  G  Y  T   F  T  N   Y  G  M   N  W  V  K   Q  A  P>

         190         200         210         220         230         240
           *           *           *           *           *           *
GGAAAGGGTT TAAAGTGGAT GGGCTGGATA AACACCAAGA GTGGAGAGCC AACATATGCT
 G  K  G   L  K  W  M   G  W  I   N  T  K   S  G  E  P   T  Y  A>

         250         260         270         280         290         300
           *           *           *           *           *           *
GAAGAGTTCA AGGGACGGTT TGCCTTCTCT TTGGAAACCT CTGCCAGCAC TGCCAATTTG
 E  E  F   K  G  R  F   A  F  S   L  E  T   S  A  S  T   A  N  L>

         310         320         330         340         350         360
           *           *           *           *           *           *
CAGATCAAGA ACCTCAAAAA TGAGGACACG GCTACATATT TCTGTGCAAG ATGGGTACCT
 Q  I  K   N  L  K  N   E  D  T   A  T  Y   F  C  A  R   W  V  P>

         370         380         390         400         410
           *           *           *           *           *
GGGACCTATG CCATGGACTA CTGGGGTCAA GGAACCTCAG TCACCGTCTC CTCA
 G  T  Y   A  M  D  Y   W  G  Q   G  T  S   V  T  V  S   S
```

h77A3-1 and h77A3-2 LIGHT CHAIN

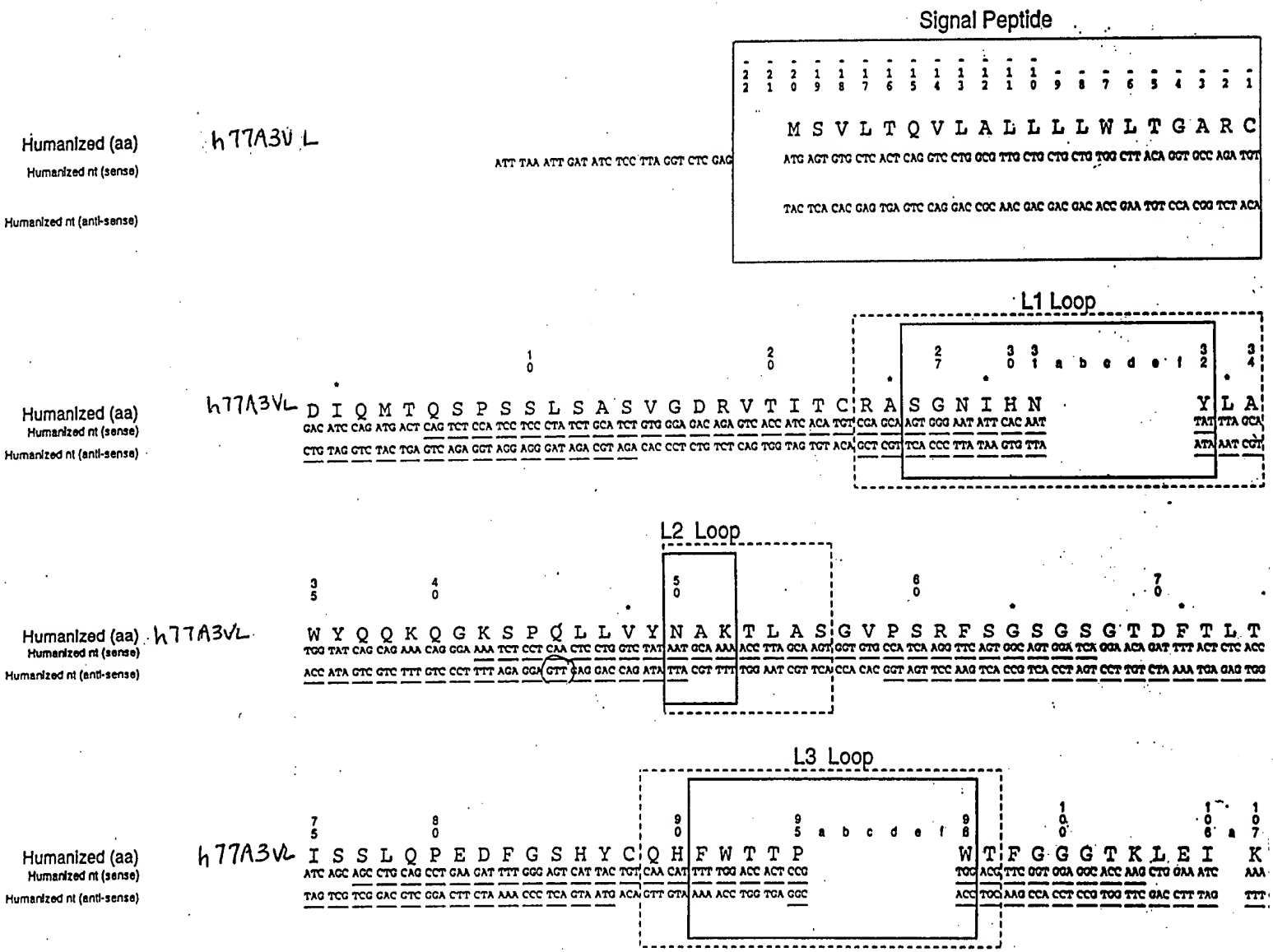

Figure 17

h77A3-1 HEAVY CHAIN SEQUENCES

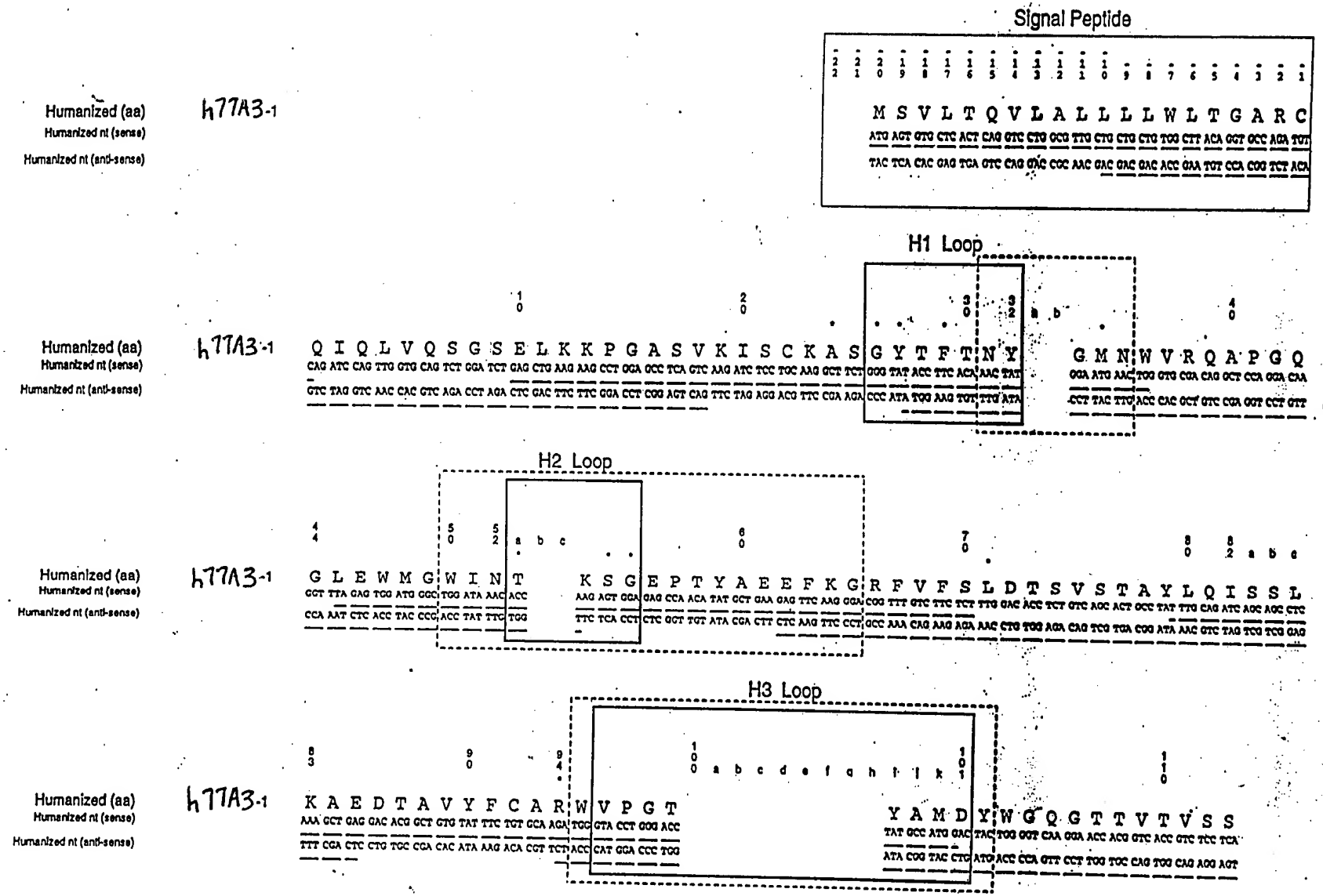

Figure 16

h77A3-2 HEAVY CHAIN SEQUENCES

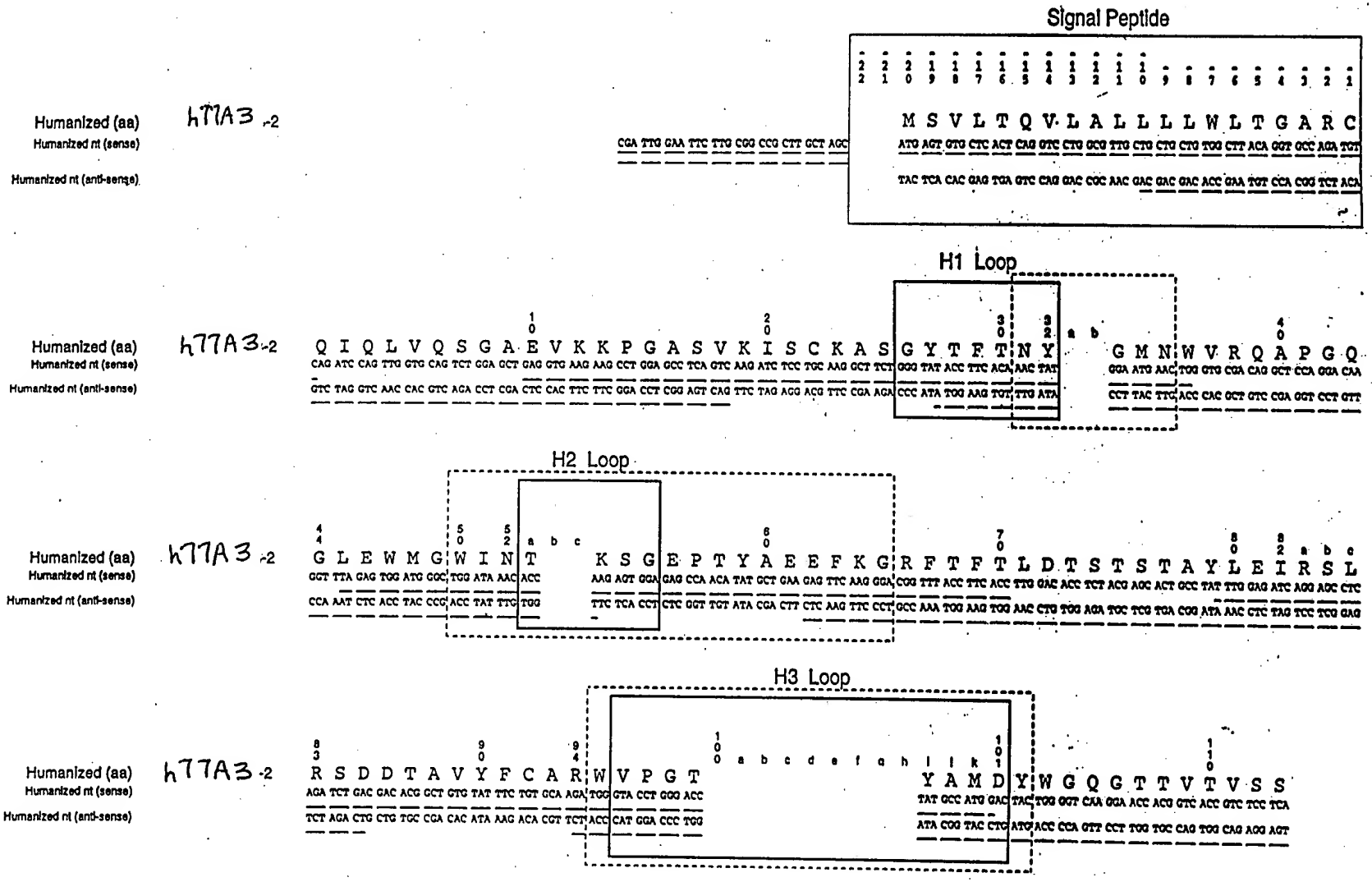

Figure 19

Figure 20

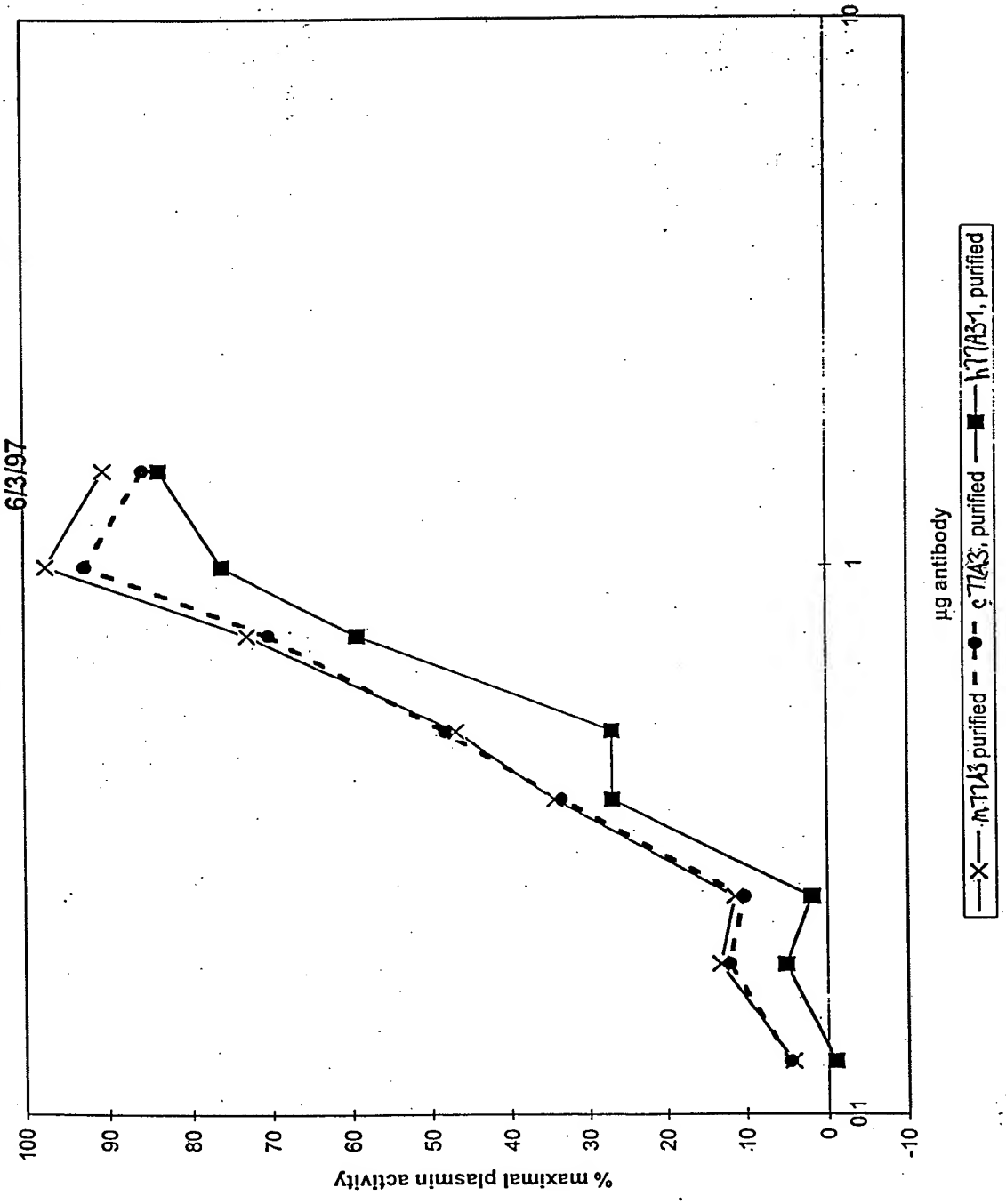
Plasmin Assay
Murine, Chimeric and Humanized 7A3
6/3/97
% maximal plasmin activity
100
90
80
70
60
50
40
30
20
10
0
-10
0.1
1
10
µg antibody
m7A3 purified
c7A3, purified
h7A3-1, purified

Figure 21

α2-antiplasmin antibody light chain sequences

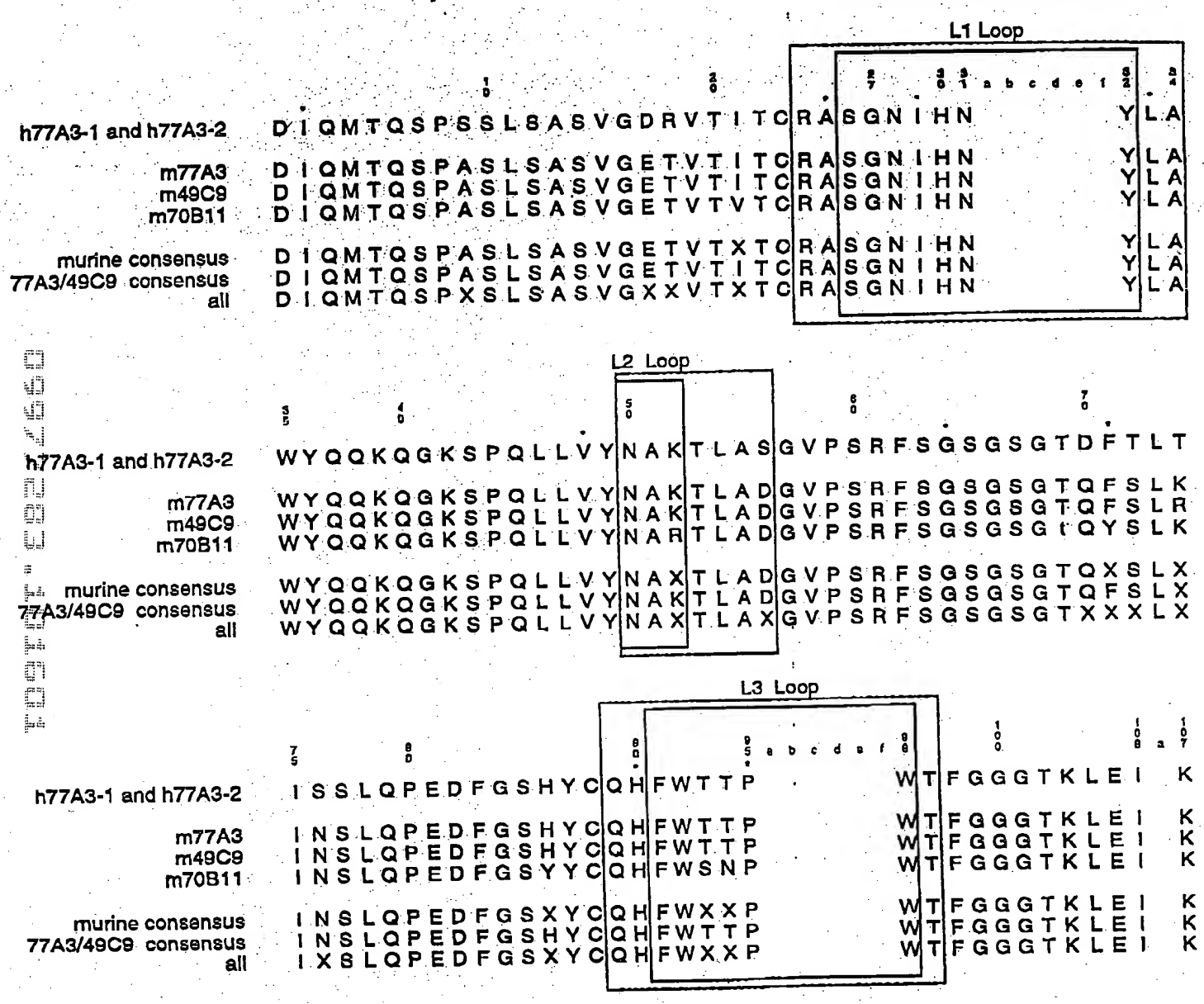

Figure 22

α2-antiplasmin antibody heavy chain sequences